

In the Claims,

1-16 (Canceled).

17. (New) A method for identifying a molecular interaction network of interacting molecules for a set of molecules within a biological system, wherein said interacting molecules have one or more conserved features, said method comprising:

- a) determining attraction probabilities between said conserved features of different molecules within the set of molecules based on known molecular interaction networks;
- b) determining a single network probability of each possible network based on a molecular interaction probability of each pair of the reacting molecules within said each network, wherein said molecular interaction probability is determined by using the attraction probabilities between features of the interacting molecules;
- c) determining a sampling probability of said each network based on network topology of said each network;
- d) determining a network probability of each network as a product of said single network probability and said sampling probability; and
- e) identifying the network having the highest network probability as the molecular interaction network of interacting molecules for the set of molecules.

18. (New) The method of claim 17, wherein said attraction probabilities between said conserved features are determined by quantifying the occurrence frequency of said features at immediate upstream or downstream of each other within the known networks.

19. (New) The method of claim 1, wherein said attraction probabilities of said features are determined by using equation 6 or 14.

20. (New) The method of claim 17, wherein said attraction probabilities of said features are determined by using equation 14.

21. (New) The method of claim 17, wherein said molecular interaction probability of each pair of reacting molecules is determined by using equation 5 or 17.

22. (New) The method of claim 17, wherein said molecular interaction probability of each pair of reacting molecules is determined by equation 17.

23. (New) The method of claim 17, wherein said sampling probability of each possible network is a product of incoming edge distribution probability and outgoing edge distribution probability within said each possible network.
24. (New) The method of claim 17, further comprising step of obtaining posterior probability of each network, wherein said molecular interaction network having the highest network probability is the network having the highest posterior probability.
25. (New) The method of claim 24, wherein said posterior probability is determined by using Markov Chain Monte Carlo techniques.
26. (New) The method of claim 17, wherein said interacting molecules are proteins and said conserved features are protein domains or motifs.
27. (New) The method of claim 26, wherein said conserved features are nucleic acid motifs.
28. (New) The method of claim 26, wherein said probabilities between said conserved features are determined by quantifying the occurrence frequency of said features at immediate upstream or downstream of each other within the known networks; and said molecular interaction probability of each pair of reaction molecules is determined by using equation 6 or 14.
29. (New) The method of claim 26, wherein said molecular interaction probability is determined by using equation 5
30. (New) The method of claim 26, wherein said topology probability of each possible network is a product of incoming edge distribution probability and outgoing edge distribution probability within said each possible network; and further comprising step of obtaining posterior probability of each network, wherein said molecular interaction network having the highest network probability is the network having the highest posterior probability, wherein said highest posterior probability is determined by Markov Chain Monte Carlo techniques.
31. (New) The method of claim 30, wherein said attraction probabilities of said features are determined by using equation 6 or 14.
32. (New) The method of claim 30, wherein said attraction probabilities of said features are determined by using equation 14.
33. (New) The method of claim 30, wherein said molecular interaction probability of each pair of reacting molecules is determined by using equation 5 or 17.
34. (New) The method of claim 30, wherein said molecular interaction probability of each pair of reacting molecules is determined by equation 17.

35. (New) A method for identifying a molecular interaction network of interacting molecules for a set of molecules within a known biological system, wherein said interacting molecules have one or more conserved features , said method comprising:
- a. determining attraction probabilities between said conserved features of different molecules of the set of molecules based on known molecular interaction data where said attraction probabilities are determined by quantifying the occurrence frequency of said features at immediate upstream or downstream of each other within the known networks and using equation 6 or 14;
 - b. determining a single network probability of each possible network based on molecular interaction probabilities of each pair of reaction molecules within said each network using equation 5 or 17;
 - c. determining sampling probability of said each network based on the network topology of said each network, said sampling probability being a product of incoming edge distribution probability and outgoing edge distribution probability within said each possible network.
 - d. determining a network probability of each network as a product of said single network probability and said topology probability;
 - e. determining a posterior probability of said each network using equation 10; and
 - f. identifying the network having the highest posterior probability as said molecular interaction network of interacting molecules for the set of molecules.
36. (New) The method of Claim 35, wherein said molecules are protein and said conserved features are protein domain or motif.
37. (New) A method for identifying a molecular interaction of a molecule within a biological network wherein said biological network comprises a set of interacting molecules and said interacting molecules have one or more conserved features, said method comprising:
- a. identifying a conserved feature of said molecule
 - b. determining attraction probabilities between the conserved features of said molecule and the interacting molecules based on known molecular interaction data of the biological network;

- c. determining molecular probabilities of said molecule with each of the interacting molecules based on the attraction probabilities; and
 - d. identifying the molecular interaction of said molecule with a interacting molecule, which provides highest molecular probability with said molecule.
38. (New) The method of claim 37, wherein said attraction probabilities of said features are determined by using equation 6 or 14.
39. (New) The method of claim 37, wherein said attraction probabilities of said features are determined by using equation 14.
40. (New) The method of claim 37, wherein said molecular probability of the molecular interaction between said two molecules is identified by using equations 5 or 17.
41. (New) The method of claim 37, wherein said likelihood of molecular interactions between said interacting molecules is determined by using equations 17.
42. (New) The method of claim 37, wherein said molecules are protein, and said conserved features are protein domain or motif.
43. (New) A screening method for identification of a compound capable of modifying the interaction between at least two molecules with a biology network comprising
- a. identifying an interaction between said at least two molecules using the method of claim 37;
 - b. contacting said proteins identified in step (a) with a test compound;
 - c. comparing the interaction of the molecules in the presence of the test compound with the interaction in the absence of the test compound;
- wherein a difference in the interaction of the molecules in the presence of the test compound as compared to the interaction in the absence of a test compound indicates identification of a compound capable of modifying the interaction between molecules.
44. (New) The screening method of claim 43, wherein said molecules are proteins.